

GenCore version 5.1.4-p5-578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:00:40 ; Search time 29.3505 Seconds

(without alignments)
2351.779 Million cell updates/sec

Title: US-09-446-634A-22

Perfect score: 1804

Sequence: 1 MGJITPLPLVTSVRLSS.....KDTSDSENSEFRIETOSLY 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:
2: SP_BACTERIA:
3: SP_FUNGI:
4: SP_HUMAN:
5: SP_INVERTEBRATE:
6: SP_MAMMAL:
7: SP_MHC:
8: SP_ORNITHINE:
9: SP_PLANT:
10: SP_PROTOZOA:
11: SP_VIRUS:
12: SP_VIRUS:
13: SP_VIRUS:
14: SP_VIRUS:
15: SP_VIRUS:
16: SP_VIRUS:
17: SP_VIRUS:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1552	86.0	331	6	O9TSM4 macaca fasc
2	1531	84.9	331	6	O9BDN0 macaca neme
3	1521	84.3	331	6	O9BDN4 macaca neme
4	1509	83.6	333	6	O9BDP2 macaca mola
5	1500	83.1	331	6	O9GK36 macaca aspa
6	1492.5	82.7	334	6	O9GK40 macaca mola
7	1439.5	79.8	310	6	O9GK28 macaca arc
8	1377.5	76.4	328	6	O9GK28 macaca arc
9	1057.5	58.3	320	6	O9XS29 macaca arc
10	1052	58.3	319	6	O9XS29 macaca arc
11	967	53.6	327	6	O9TSM4 macaca fasc
12	614.5	34.1	263	6	O9XS60 macaca arc
13	481.5	26.7	150	11	O9R230 macaca arc
14	478	26.3	147	6	O9S032 macaca arc
15	470	26.1	285	13	O9DGH7 macaca arc
16	463.5	25.7	312	13	O9DGH8 macaca arc

17	429.5	23.8	124	6	O9S031 macaca arc
18	286	15.9	65	6	O9S049 macaca arc
19	246	13.6	357	13	O9DGH3 macaca arc
20	226.5	12.6	368	13	O9DGH3 macaca arc
21	212.5	11.8	438	13	O9DGH3 macaca arc
22	208.5	11.6	387	13	O9DGH3 macaca arc
23	199	11.0	368	13	O9DGH3 macaca arc
24	198	11.0	383	6	O9XS28 macaca arc
25	189	10.5	368	13	O9DGH3 macaca arc
26	180	10.0	276	13	O9DGH3 macaca arc
27	179	9.9	401	13	O9DGH3 macaca arc
28	171	9.5	413	11	O9S041 macaca arc
29	170.5	9.5	446	6	O9S041 macaca arc
30	168	9.3	186	12	O9S041 macaca arc
31	163	9.0	186	12	O9S041 macaca arc
32	161.5	9.0	169	11	O9S041 macaca arc
33	161.5	9.0	326	12	O9S041 macaca arc
34	161	8.9	186	12	O9S041 macaca arc
35	161	8.9	186	12	O9S041 macaca arc
36	159.5	8.8	350	12	O9S041 macaca arc
37	158.5	8.8	278	6	O9S041 macaca arc
38	155.5	8.6	387	11	O9S041 macaca arc
39	153.5	8.5	326	12	O9S041 macaca arc
40	153	8.5	349	12	O9S041 macaca arc
41	153	8.5	349	12	O9S041 macaca arc
42	153	8.5	349	12	O9S041 macaca arc
43	152	8.4	347	12	O9S041 macaca arc
44	151.5	8.4	349	12	O9S041 macaca arc
45	151.5	8.4	349	12	O9S041 macaca arc

ALIGNMENTS

RESULT 1					
ID	O9TSM4	PRELIMINARY:	PRT:	331 AA.	
AC	O9TSM4				
DT	01-MAR-2000 (TREMUR)				
DT	01-MAR-2000 (TREMUR)				
DT	01-DEC-2001 (TREMUR)				
DE	Death receptor Fas (APO-1/CD95).				
GN	FAS.				
OS	Macaca fascicularis (Crib eating macaque) (Cynomolgus monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;				
OC	Cercopithecoidea; Macaca.				
OX	NCBI_TaxID:9541;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-20237686; PubMed-10773350;				
RA	Murayama Y., Terao K., Inoue-Murayama M.;				
RT	"Molecular cloning and characterization of cynomolgus monkey Fas.";				
RL	Hum. Immunol. 61:474-485(2000).				
DR	EMBL: AB031430; BAA83551.1; -				
DR	SSSP: P25445; IDDF.				
DR	InterPro: IPR000488; Death.				
DR	InterPro: IPR001368; TNFR-C6.				
DR	Pfam: PF00531; death_1.				
DR	Pfam: PF00020; TNFR_C6; 2.				
DR	SMART: SM00005; DEATH_1.				
DR	SMART: SM00005; TNFR_2.				
DR	PROSITE: PSS0017; DEATH_DOMAIN; 1.				
DR	PROSITE: PSS0052; TNFR_NGFR_1; 1.				
DR	PROSITE: PSS0050; TNFR_NGFR_2; 2.				
KW	Receptor.				
SO	SEQUENCE				
	331 AA; 37265 MW; 06617508081B05DF CRC64;				
Query Match	86.0%; Score 1552; DB 6; Length 331;				
Best Local Similarity	87.2%; Pred. No. 2.2e-121;				
Matches 292; Conservative	14; Mismatches 25; Indels 4; Gaps 2;				
OY	1 MGJITPLPLVTSVRLSSVNAQVTDINSKLEIRKTVTVETONLECHHDCQFCH 60				

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OM protein - protein search, using SW model

Run on: May 9, 2003, 17:02:31; Search time 28.1556 seconds
(without alignments)
1116.509 Million cell updates/sec

Title: US-09-446-634A-23
Perfect score: 1804
Sequence: 1 MIMINAVLPVLVAGSQLRVH.....KDLGKSPDTGNEGQGLE 327

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_73:*

- 1: PIR1:*
- 2: PIR2:*
- 3: PIR3:*
- 4: PIR4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1804	100.0	327	2	A66484
2	1058.5	58.7	324	2	JC2395
3	856	47.5	335	2	A40036
4	810.5	44.9	314	2	I37383
5	305.5	16.9	149	2	S58662
6	203.5	11.3	271	2	S12783
7	202	11.2	272	2	I48700
8	194.5	10.8	277	2	A60771
9	189.5	10.5	455	1	GOHRT1
10	185	10.3	454	1	GOHRT1
11	183	10.1	260	1	A46517
12	179.5	10.0	435	2	I35182
13	179	9.9	461	1	GOHRT1
14	171	9.5	277	2	I37552
15	169	9.4	461	2	JC4302
16	167	9.3	250	1	A49053
17	165.5	9.2	416	1	JN0006
18	165	9.1	305	2	A46476
19	165	9.1	349	2	D72175
20	163	9.0	348	2	T28623
21	163	9.0	349	2	D36558
22	154.5	8.6	425	1	A26431
23	154.5	8.6	595	2	A42086
24	148	8.2	461	1	A35356
25	141	7.8	427	1	GOHUN
26	135.5	7.5	677	2	C42125
27	126.5	7.0	1372	2	T25933
28	126	7.0	493	2	JC5486
29	123.5	6.8	459	2	I4854

30	122.5	6.8	255	2	I38426
31	122	6.8	103	2	I37384
32	120.5	6.7	1111	2	T26972
33	119.5	6.6	474	2	B38634
34	119	6.6	2823	2	T23004
35	119	6.6	2823	2	F87908
36	119	6.6	3102	2	T43291
37	116.5	6.5	325	2	B43692
38	116	6.4	3712	2	S18253
39	115.5	6.4	1820	2	T27283
40	115.5	6.4	1816	1	S68960
41	115.5	6.4	3672	2	T23433
42	115.5	6.4	3704	2	T27316
43	115	6.4	1274	2	T42017
44	114	6.3	626	2	T04895
45	114	6.3	686	2	JC7569

lymphocyte activat
FAS soluble protei
hypothetical prote
tumor necrosis fac
hypothetical prote
protein T22A3.8 (1
laminin alpha chain
laminin alpha-1 ch
hypothetical prote
laminin alpha-4 ch
hypothetical prote
probable laminin a
cysteine rich prot
vacuolar sorting r
Delta-4 protein -

ALIGNMENTS

RESULT 1
A66484
A:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence revision 18-Nov-1994 #text change 05-Nov-1999
C:Accession: A46484; A47254
R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenk
J. Immunol. 148, 1274-1279, 1992
A:Title: The CDNA structure, expression, and chromosomal assignment of the mouse Fas
A:Reference number: A46484; MUID:9218151; PMID:1371136
A:Accession: A46484
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1327<KAT>
A:Cross-References: GB:M3649; NID:919325; PID:AAA37593.1; PID:9193226
A:Experimental source: EMB3 macrophage cell line
A:Note: Sequence extracted from NCBI backbone (NCBIN:81544, NCBI:81545)
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A:Title: Aberrant transcription caused by the insertion of an early transposable ele
F:44-79/Domain: NSf receptor repeat homology <NGF>
A:Reference number: A47254; MUID:93189576; PMID:7680478
A:Accession: A47254
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 196<ADA>
A:Cross-References: GB:S56490; NID:9298505; PID:AA825700.1; PID:9298506
A:Experimental source: MRL lpr/lpr
A:Note: Sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126
C:Superfamily: NGF receptor repeat homology
C:Keywords: transmembrane protein
F:44-79/Domain: NSf receptor repeat homology <NGF>
F:81-124/Domain: NGF receptor repeat homology <NGF>
Query Match 100.0%; Score 1804; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 6.9e-122;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MIMINAVLPVLVAGSQLRVHVTGNTSISLKLRRVETDKNSBGLYGGFFCQPCQ 60
1 MIMINAVLPVLVAGSQLRVHVTGNTSISLKLRRVETDKNSBGLYGGFFCQPCQ 60
61 PGKRYEDCKNMGTPCAPCTGKREYMDKNHAKRCYLCDEHGLEVFNCTN 120
61 PGKRYEDCKNMGTPCAPCTGKREYMDKNHAKRCYLCDEHGLEVFNCTN 120
121 TKCKCPDYDSCRCCHYRACSCHGTECTTSNTNCRKOSPNNRLMLTLIVLI 180
121 TKCKCPDYDSCRCCHYRACSCHGTECTTSNTNCRKOSPNNRLMLTLIVLI 180
181 PLVFYRKYRKRKCKRRRDPESRTSSRETIIPNANSLSLSKYIPRIADMTYCAKF 240
181 PLVFYRKYRKRKCKRRRDPESRTSSRETIIPNANSLSLSKYIPRIADMTYCAKF 240

